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GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTORS.

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- (73) Proprietor: **IMMUNEX CORPORATION**
Immunex Building
51 University Street
Seattle, WA 98101 (US)
- (72) Inventor: **SMITH, Craig, A.**
2405 5th West
Seattle, WA 98119 (US)
Inventor: **LARSEN, Alf, D.**
320 Summit Avenue East, 15
Seattle, WA 98104 (US)
Inventor: **SIMS, John, E.**
314 Northeast 82nd Street
Seattle, WA 98115 (US)
Inventor: **CURTIS, Benson, M.**
1520 Northwest Woodbine Way
Seattle, WA 98177 (US)
- (74) Representative: **Froud, Clive et al**
Elkington and Fife
Prospect House
8 Pembroke Road
Sevenoaks, Kent TN13 1XR (GB)

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Description**CROSS-REFERENCE TO RELATED APPLICATION**

- 5 This application is a continuation-in-part of U.S. Application Serial No. 522,952, filed April 3, 1990, which is a continuation-in-part of U.S. Application Serial No. 416,306, filed October 3, 1989, which is a continuation-in-part of U.S. Application Serial No. 412,816, filed on September 26, 1989.

BACKGROUND OF THE INVENTION

- 10 The present invention relates generally to cytokine receptors and more specifically to granulocyte-colony stimulating factor receptors.

- Human Granulocyte-Colony Stimulating Factor (G-CSF) is a lineage-specific hematopoietic protein which stimulates the proliferation and differentiation of granulocyte-committed progenitor cells. Human G-CSF has also been shown to functionally activate mature neutrophils. The cDNAs for human (Nagata et al., *Nature* 319:415, 1986) and mouse G-CSF (Tsuchiya et al., *PNAS* 83, 7633, 1986) have been isolated, permitting further structural and biological characterization of G-CSF.

- G-CSF initiates its biological effect on cells by binding to specific G-CSF receptor protein expressed on the plasma membrane of a G-CSF responsive cell. Because of the ability of G-CSF to specifically bind G-CSF receptor (G-CSFR), purified G-CSFR compositions will be useful in diagnostic assays for G-CSF, as well as in raising antibodies to G-CSF receptor for use in diagnosis and therapy. In addition, purified G-CSF receptor compositions may be used directly in therapy to bind or scavenge G-CSF, thereby providing a means for regulating the immune activities of this cytokine. In order to study the structural and biological characteristics of G-CSFR and the role played by G-CSFR in the responses of various cell populations to G-CSF or other cytokine stimulation, or to use G-CSFR effectively in therapy, diagnosis, or assay, purified compositions of G-CSFR are needed. Such compositions, however, are obtainable in practical yields only by cloning and expressing genes encoding the receptors using recombinant DNA technology. Efforts to purify the G-CSFR molecule for use in biochemical analysis or to clone and express mammalian genes encoding G-CSFR have been impeded by lack of a suitable source of receptor protein or mRNA. Prior to the present invention, no cell lines were known to express high levels of G-CSFR constitutively and continuously, which precluded purification of receptor for sequencing or construction of genetic libraries for direct expression cloning.

SUMMARY OF THE INVENTION

- 35 The present invention provides DNA sequences encoding mammalian granulocyte-colony stimulating factor receptors (G-CSFR) or subunits thereof. Preferably, such DNA sequences are selected from the group consisting of (a) cDNA clones having a nucleotide sequence derived from the coding region of a native G-CSFR gene; (b) DNA sequences which are capable of hybridization to the cDNA clones of (a) under moderately stringent conditions and which encode biologically active G-CSFR molecules; and (c) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (a) and (b) and which encode biologically active G-CSFR molecules. The present invention also provides recombinant expression vectors comprising the DNA sequences defined above, recombinant G-CSFR molecules produced using the recombinant expression vectors, and processes for producing the recombinant G-CSFR molecules using the expression vectors.

The present invention also provides isolated or purified protein compositions comprising mammalian G-CSFR. Preferred G-CSFR proteins are soluble forms of the native receptors.

- The present invention also provides compositions for use in therapy, diagnosis, assay of G-CSFR, or in raising antibodies to G-CSFR, comprising effective quantities of soluble native or recombinant receptor proteins prepared according to the foregoing processes. These and other aspects of the present invention will become evident upon reference to the following detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

- 55 FIGURE 1 shows restriction maps of cDNA clones D-7 and 25-1 containing regions encoding human G-CSFR proteins.

FIGURES 2-5 depict that cDNA sequence of clone D-7 which was isolated from a human placental library, and the predicted amino acid sequence of this clone. The coding region of the predicted mature full-

length membrane-bound protein from clone D7 is defined by amino acids 1-759. The predicted N-terminal Glu of the mature protein is designated amino acid number 1 and is underlined. The putative transmembrane region at amino acids 604-629 is also underlined.

FIGURE 6 depicts the 3' nucleotide sequence and predicted C-terminal amino acid sequence of clone 25-1, which is the result of an alternative splicing arrangement. The position of the intron insertion in clone 25-1 is indicated with a ↓ after nucleotide 2411 of Figure 1. The position of the intron-exon boundaries are indicated with a ↓, and splice-donor and splice-acceptor recognition sequences are boxed. Sequences also present in clone D-7 are underlined.

10 DETAILED DESCRIPTION OF THE INVENTION

Definitions

G-CSF is a growth factor which induces growth and differentiation of neutrophilic granulocyte progenitors. The biological activities of G-CSF are mediated through binding to specific cell surface receptors, referred to as "G-CSF receptors" or "G-CSFR". G-CSFR, as used herein, refers to proteins having amino acid sequences which are substantially similar to native mammalian G-CSFR amino acid sequences, such as the human G-CSFR sequence disclosed in Figures 2-5, or fragments thereof, and which are biologically active as defined below, in that they are capable of binding G-CSF molecules or, in their native configuration as intact human plasma membrane proteins, transducing a biological signal initiated by a G-CSF molecule binding to a cell, or cross-reacting with anti-G-CSFR antibodies raised against G-CSFR from natural (i.e., nonrecombinant) sources. Specific embodiments of G-CSFR include polypeptides substantially equivalent to the sequence of amino acids 1-759 of Figures 2-5 (clone D-7) or the sequence of amino acids 1-776 of the protein encoded by clone 25-1 as disclosed in Figures 2-5 and 6. The terms "G-CSF receptor" or "G-CSFR" include, but are not limited to, soluble G-CSF receptors, as defined below. As used throughout this specification, the term "mature" means a protein expressed in a form lacking a leader sequence as may be present in full-length transcripts of a native gene. Various bioequivalent protein and amino acid analogs are described in detail below.

The mature N-terminal amino acid is predicted to be Glu¹ (underlined and designated as amino acid 1 in Figures 2-5), based on the algorithm of von Heijne, G., *Nucl. Acids Res.* 14:4683 (1986), for determining signal cleavage sites. However, several factors suggest that Ser⁻³ may be the correct mature N-terminal amino acid, based on the observation that Ser⁻³ is 21 amino acids from the N-terminal Met and is preceded by the small amino acid residue Gly, both of which are accepted criteria for identifying signal cleavage sites. The actual N-terminal amino acid of the mature protein can be confirmed by sequencing purified G-CSFR protein using standard techniques. Thus, amino acid sequences equivalent to those described above include, for example, amino acids -3 through 759 of Figures 2-5 (clone D-7) or -3 through 776 of the protein encoded by clone 25-1 as disclosed in Figures 2-5 and 6.

In their native configuration, receptor proteins are present as intact human plasma membrane proteins having an extracellular region which binds to a ligand, a hydrophobic transmembrane region which causes the protein to be immobilized within the plasma membrane lipid bilayer, and a cytoplasmic or intracellular region which interacts with cytoplasmic proteins and/or chemicals to deliver a biological signal to effector cells via a cascade of chemical reactions within the cytoplasm of the cell. The hydrophobic transmembrane region and a highly charged sequence of amino acids in the cytoplasmic region immediately following the transmembrane region cooperatively function to halt transport of the G-CSFR across the plasma membrane. "Soluble G-CSFR" or sG-CSFR", as used in the context of the present invention, refer to a protein, or a substantially equivalent analog, having an amino acid sequence corresponding to the extracellular region of native G-CSFR, for example polypeptides having the amino acid sequences substantially equivalent to the sequences of amino acids 1-603 of Figures 2-5. Equivalent sG-CSFRs include polypeptides which vary from the sequences shown in Figures 2-5 by one or more substitutions, deletions, or additions, and which retain the ability to bind G-CSF and inhibit the ability of G-CSF to transduce a signal via cell surface bound G-CSF receptor proteins. Because sG-CSFR proteins are devoid of a transmembrane region, they are secreted from the host cell in which they are produced. Equivalent soluble G-CSFR include, for example, the sequence of amino acids -3 through 603 of Figures 2-5. When administered in therapeutic formulations, sG-CSFR proteins circulate in the body and bind to circulating G-CSF molecules, preventing interaction of G-CSF with natural G-CSF receptors and inhibiting transduction of G-CSF-mediated biological signals, such as immune or inflammatory responses. The ability of a polypeptide to inhibit G-CSF signal transduction can be determined by transfecting cells with recombinant G-CSF receptor DNAs to obtain recombinant receptor expression. The cells are then contacted with G-CSF and the resulting metabolic effects examined. If an

effect results which is attributable to the action of the ligand, then the recombinant receptor has signal transducing activity. Exemplary procedures for determining whether a polypeptide has signal transducing activity are disclosed by Idzerda et al., *J. Exp. Med.* 171:861 (1990); Curtis et al., *Proc. Natl. Acad. Sci. USA* 86:3045 (1989); Prywes et al., *EMBO J.* 5:2179 (1986); and Chou et al., *J. Biol. Chem.* 262:1842 (1987). Alternatively, primary cells of cell lines which express an endogenous G-CSF receptor and have a detectable biological response to G-CSF could also be utilized.

"Substantially similar" G-CSFR include those whose amino acid or nucleic acid sequences vary from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which is to retain biological activity of the G-CSFR protein. Alternatively, nucleic acid subunits and analogs are "substantially similar" to the specific DNA sequences disclosed herein if: (a) the DNA sequence is derived from the coding region of a native mammalian G-CSFR gene; (b) the DNA sequence is capable of hybridization to DNA sequences of (a) under moderately stringent conditions and which encode biologically active G-CSFR molecules; or DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (a) or (b) and which encode biologically active G-CSFR molecules. Substantially similar analog proteins will be greater than about 30 percent similar to the corresponding sequence of the native G-CSFR. Sequences having lesser degrees of similarity but comparable biological activity are considered to be equivalents. More preferably, the analog proteins will be greater than about 80 percent similar to the corresponding sequence of the native G-CSFR, in which case they are defined as being "substantially identical." In defining nucleic acid sequences, all subject nucleic acid sequences capable of encoding substantially similar amino acid sequences are considered substantially similar to a reference nucleic acid sequence. Percent similarity may be determined, for example, by comparing sequence information using the GAP computer program, version 6.0, available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443, 1970), as revised by Smith and Waterman (*Adv. Appl. Math.* 2:482, 1981). Briefly, the GAP program defines similarity as the number of aligned symbols (i.e., nucleotides or amino acids) which are similar, divided by the total number of symbols in the shorter of the two sequences. The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess, *Nucl. Acids Res.* 14:6745, 1986, as described by Schwartz and Dayhoff, ed., *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, pp. 353-358, 1979; (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

"Recombinant," as used herein, means that a protein is derived from recombinant (e.g., microbial or mammalian) expression systems. "Microbial" refers to recombinant proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a protein produced in a microbial expression system which is essentially free of native endogenous substances. Protein expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycan. Protein expressed in yeast may have a glycosylation pattern different from that expressed in mammalian cells.

"Biologically active," as used throughout the specification as a characteristic of G-CSF receptors, means that a particular molecule shares sufficient amino acid sequence similarity with the embodiments of the present invention disclosed herein to be capable of binding detectable quantities of G-CSF, transmitting a G-CSF stimulus to a cell, for example, as a component of a hybrid receptor construct, or cross-reacting with anti-G-CSFR antibodies raised against G-CSFR from natural (i.e., nonrecombinant) sources. Preferably, biologically active G-CSF receptors within the scope of the present invention are capable of binding greater than 0.1 nmoles G-CSF per nmole receptor, and most preferably, greater than 0.5 nmole G-CSF per nmole receptor in standard binding assays (see below).

"DNA sequence" refers to a DNA polymer, in the form of a separate fragment or as a component of a larger DNA construct, which has been derived from DNA isolated at least once in substantially pure form, i.e., free of contaminating endogenous materials and in a quantity or concentration enabling identification, manipulation, and recovery of the sequence and its component nucleotide sequences by standard biochemical methods, for example, using a cloning vector. Such sequences are preferably provided in the form of an open reading frame uninterrupted by internal nontranslated sequences, or introns, which are typically present in eukaryotic genes. Genomic DNA containing the relevant sequences could also be used. Sequences of non-translated DNA may be present 5' or 3' from the open reading frame, where the same do not interfere with manipulation or expression of the coding regions.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. DNA sequences encoding the proteins provided by this invention can be assembled from cDNA fragments and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being

expressed in a recombinant transcriptional unit.

"Recombinant expression vector" refers to a replicable DNA construct used either to amplify or to express DNA which encodes G-CSFR and which includes a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription and translation initiation and termination sequences. Structural elements intended for use in yeast expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may optionally be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant microbial expression system" means a substantially homogeneous monoculture of suitable host microorganisms, for example, bacteria such as *E. coli* or yeast such as *S. cerevisiae*, which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit as a component of a resident plasmid. Generally, cells constituting the system are the progeny of a single ancestral transformant. Recombinant expression systems as defined herein will express heterologous protein upon induction of the regulatory elements linked to the DNA sequence or synthetic gene to be expressed.

The term "isolated", as used in the context of this specification to define the purity of a G-CSFR or sG-CSFR protein or protein composition, means that the protein or protein composition is substantially free of other proteins of natural or endogenous origin and contains less than about 1% by mass of protein contaminants residual of production processes. Such compositions, however, can contain other proteins added as stabilizers, carriers, excipients or co-therapeutics. G-CSFR or sG-CSFR is isolated if it is detectable as a single protein band in a polyacrylamide gel by silver staining.

25 Isolation of cDNAs Encoding G-CSFR

The coding sequence of a mammalian G-CSFR is obtained by first isolating a cDNA sequence encoding G-CSFR from a recombinant DNA library generated using either genomic DNA or cDNA. The preferred method for constructing a cDNA library is to prepare polyadenylated mRNA obtained from a particular cell line which expresses a mammalian G-CSFR and converting the polyadenylated RNA to cDNA by reverse transcription. A particularly preferred cellular source of mRNA for construction of the cDNA library is human placental RNA.

A cDNA library will contain G-CSFR sequences which can be readily identified by screening the library with an appropriate nucleic acid probe which is capable of hybridizing with G-CSFR cDNA. Such probes can be derived from the nucleotide sequences disclosed herein. Alternatively, DNAs encoding G-CSFR proteins can also be assembled by ligation of synthetic oligonucleotide subunits to provide a complete coding sequence.

The cDNAs encoding G-CSFR of the present invention were isolated by the method of direct expression cloning. Specifically, a cDNA library was constructed by first isolating cytoplasmic mRNA from human placental tissue using standard techniques. Polyadenylated mRNA was isolated and used to prepare double-stranded cDNA. Purified cDNA fragments were then ligated into pscAV vector DNA described in detail below in Example 2. The pscAV vectors containing the G-CSFR cDNA fragments were transformed into *E. coli* strain DH5 α . Transformants were plated to provide approximately 800 colonies per plate. The resulting colonies were harvested and each pool used to prepare plasmid DNA for transfection into COS-7 cells essentially as described by Cosman et al. (*Nature* 312:768, 1984) and Luthman et al. (*Nucl. Acid Res.* 11:1295, 1983). Transformants expressing biologically active cell surface G-CSF receptors were identified by screening for the ability of G-CSFR to bind 125 I-G-CSF (5×10^{-10} M). Specifically, transfected COS-7 cells were incubated with medium containing 125 I-G-CSF, the cells washed to remove unbound labeled G-CSF, and the cell monolayers contacted with X-ray film to detect concentrations of G-CSF binding, as disclosed by Sims et al, *Science* 241:585 (1988). Transfectants detected in this manner appear as dark foci against a relatively light background.

This approach as used to screen approximately 30,000 cDNAs in pools of approximately 600 cDNAs until assay of a transfectant pool indicated positive foci for G-CSF binding. A frozen stock of bacteria from this positive pool was grown in culture and plated to provide individual colonies, which were screened until single clones were identified which are capable of directing synthesis of a surface protein with detectable G-CSF binding activity. Additional cDNA clones can be isolated from cDNA libraries of other mammalian species by cross-species hybridization of human G-CSFR cDNAs with cDNA derived from other mammalian species. For use in hybridization, DNA encoding G-CSFR may be covalently labeled with a detectable

substance such as a fluorescent group, a radioactive atom or a chemiluminescent group by methods well known to those skilled in the art. Such probes could also be used for *in vitro* diagnosis of particular conditions.

Like most mammalian genes, mammalian G-CSF receptors are presumably encoded by multi-exon genes. Alternative mRNA constructs which can be attributed to different mRNA splicing events following transcription, and which share large regions of identity or similarity with the cDNAs claimed herein, are considered to be within the scope of the present invention.

Proteins and Analogs

The present invention provides isolated recombinant mammalian G-CSFR polypeptides as defined above. Isolated G-CSFR polypeptides are substantially free of other contaminating materials of natural or endogenous origin and contain less than about 1% by mass of protein contaminants residual of production processes. Such polypeptides are optionally without associated native-pattern glycosylation. Mammalian G-CSFR of the present invention includes, by way of example, primate, human, murine, canine, feline, bovine, ovine, equine and porcine G-CSFR. Derivatives of G-CSFR within the scope of the invention also include various structural forms of the primary protein which retain biological activity. Due to the presence of ionizable amino and carboxyl groups, for example, a G-CSFR protein may be in the form of acidic or basic salts, or may be in neutral form. Individual amino acid residues may also be modified by oxidation or reduction.

The primary amino acid structure may be modified by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like, or by creating amino acid sequence mutants. Covalent derivatives are prepared by linking particular functional groups to G-CSFR amino acid side chains or at the N- or C-termini. Other derivatives of G-CSFR within the scope of this invention include covalent or aggregative conjugates of G-CSFR or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. For example, the conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast α -factor leader). G-CSFR protein fusions can comprise peptides added to facilitate purification or identification of G-CSFR (e.g., poly-His). The amino acid sequence of G-CSF receptor can also be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Lys (DYKDDDDK) (Hopp et al., *Bio/Technology* 6:1204,1988.) The latter sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. This sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing. Fusion proteins capped with this peptide may also be resistant to intracellular degradation in *E. coli*.

G-CSFR derivatives may also be used as immunogens, reagents in receptor-based immunoassays, or as binding agents for affinity purification procedures of G-CSF or other binding ligands. G-CSFR derivatives may also be obtained by cross-linking agents, such as M-maleimidobenzoyl succinimide ester and N-hydroxysuccinimide, at cysteine and lysine residues. G-CSFR proteins may also be covalently bound through reactive side groups to various insoluble substrates, such as cyanogen bromide-activated, bisoxirane-activated, carbonyldiimidazole-activated or tosyl-activated agarose structures, or by adsorbing to polyolefin surfaces (with or without glutaraldehyde cross-linking). Once bound to a substrate, G-CSFR may be used to selectively bind (for purposes of assay or purification) anti-G-CSFR antibodies or G-CSF.

The present invention also includes G-CSFR with or without associated native-pattern glycosylation. G-CSFR expressed in yeast or mammalian expression systems, e.g., COS-7 cells, may be similar or slightly different in molecular weight and glycosylation pattern than the native molecules, depending upon the expression system. Expression of G-CSFR DNAs in bacteria such as *E. coli* provides non-glycosylated molecules. Functional mutant analogs of mammalian G-CSFR having inactivated N-glycosylation sites can be produced by oligonucleotide synthesis and ligation or by site-specific mutagenesis techniques. These analog proteins can be produced in a homogeneous, reduced-carbohydrate form in good yield using yeast expression systems. N-glycosylation sites in eukaryotic proteins are characterized by the amino acid triplet Asn-A₁-Z, where A₁ is any amino acid except Pro, and Z is Ser or Thr. In this sequence, asparagine provides a side chain amino group for covalent attachment of carbohydrate. Such a site can be eliminated by substituting another amino acid for Asn or for residue Z, deleting Asn or Z, or inserting a non-Z amino acid between A₁ and Z, or an amino acid other than Asn between Asn and A₁.

G-CSFR derivatives may also be obtained by mutations of G-CSFR or its subunits. A G-CSFR mutant, as referred to herein, is a polypeptide homologous to G-CSFR but which has an amino acid sequence

different from native G-CSFR because of a deletion, insertion or substitution.

Bioequivalent analogs of G-CSFR proteins may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, aliphatic amino acid residues, such as Ile, Val, Leu or Ala may be substituted for one another, or polar amino acid residues, such as Lys and Arg, Glu and Asp, or Gln and Asn, may be substituted for one another. Also, cysteine residues can be deleted or replaced with other amino acids to prevent formation of incorrect intramolecular disulfide bridges upon renaturation. Other approaches to mutagenesis involve modification of adjacent dibasic amino acid residues to enhance expression in yeast systems in which KEX2 protease activity is present. Generally, substitutions should be made conservatively; i.e., the most preferred substitute amino acids are those having physicochemical characteristics resembling those of the residue to be replaced. Similarly, when a deletion or insertion strategy is adopted, the potential effect of the deletion or insertion on biological activity should be considered.

Subunits of G-CSFR may be constructed by deleting terminal or internal residues or sequences. Particularly preferred subunits include those in which the transmembrane region and intracellular domain of G-CSFR are deleted or substituted with hydrophilic residues to facilitate secretion of the receptor into the cell culture medium. The resulting protein is a soluble truncated G-CSFR molecule which may retain its ability to bind G-CSF.

Mutations in nucleotide sequences constructed for expression of analog G-CSFR must, of course, preserve the reading frame phase of the coding sequences and preferably will not create complementary regions that could hybridize to produce secondary mRNA structures such as loops or hairpins which would adversely affect translation of the receptor mRNA. Although a mutation site may be predetermined, it is not necessary that the nature of the mutation *per se* be predetermined. For example, in order to select for optimum characteristics of mutants at a given site, random mutagenesis may be conducted at the target codon and the expressed G-CSFR mutants screened for the desired activity.

Not all mutations in the nucleotide sequence which encodes G-CSFR will be expressed in the final product, for example, nucleotide substitutions may be made to enhance expression, primarily to avoid secondary structure loops in the transcribed mRNA (see EPA 75,444A, incorporated herein by reference), or to provide codons that are more readily translated by the selected host, e.g., the well-known *E. coli* preference codons for *E. coli* expression.

Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion.

Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene having particular codons altered according to the substitution, deletion, or insertion required. Exemplary methods of making the alterations set forth above are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 1985, 12-19); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); and U.S. Patent Nos. 4,518,584 and 4,737,462 disclose suitable techniques, and are incorporated by reference herein.

Expression of Recombinant G-CSFR

The present invention provides recombinant expression vectors which include synthetic or cDNA-derived DNA fragments encoding mammalian G-CSFR or bioequivalent analogs operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral or insect genes. Such regulatory elements include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation, as described in detail below. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants may additionally be incorporated. DNA regions are operably linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operably linked to DNA for a polypeptide if it is expressed as a precursor which participates in the secretion of the polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation. Generally, operably linked means contiguous and, in the case of secretory leaders, contiguous and in reading frame.

DNA sequences encoding mammalian G-CSF receptors which are to be expressed in a microorganism will preferably contain no introns that could prematurely terminate transcription of DNA into mRNA; however, premature termination of transcription may be desirable, for example, where it would result in mutants having advantageous C-terminal truncations, for example, deletion of a transmembrane region to yield a soluble receptor not bound to the cell membrane. Due to code degeneracy, there can be considerable variation in nucleotide sequences encoding the same amino acid sequence. Other embodiments include sequences capable of hybridizing to the sequences of the provided cDNA under moderately stringent conditions (50°C, 2 X SSC) and other sequences hybridizing or degenerate to those which encode biologically active G-CSF receptor polypeptides.

Transformed host cells are cells which have been transformed or transfected with G-CSFR vectors constructed using recombinant DNA techniques. Transformed host cells ordinarily express G-CSFR, but host cells transformed for purposes of cloning or amplifying G-CSFR DNA do not need to express G-CSFR. Expressed G-CSFR will be deposited in the cell membrane or secreted into the culture supernatant, depending on the G-CSFR DNA selected. Suitable host cells for expression of mammalian G-CSFR include prokaryotes, yeast or higher eukaryotic cells under the control of appropriate promoters. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include established cell lines of mammalian origin as described below. Cell-free translation systems could also be employed to produce mammalian G-CSFR using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels et al. (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985), the relevant disclosure of which is hereby incorporated by reference.

Prokaryotic expression hosts may be used for expression of G-CSFR that do not require extensive proteolytic and disulfide processing. Prokaryotic expression vectors generally comprise one or more phenotypic selectable markers, for example a gene encoding proteins conferring antibiotic resistance or supplying an autotrophic requirement, and an origin of replication recognized by the host to ensure amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

Useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA) and pCAV/NOT (ATCC Accession No. 68014. These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. *E. coli* is typically transformed using derivatives of pBR322, a plasmid derived from an *E. coli* species (Boliar et al., *Gene* 2:95,1977). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells.

Promoters commonly used in recombinant microbial expression vectors include the β -lactamase (penicillinase) and lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), the tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EPA 36,776) and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful bacterial expression system employs the phage λ P_L promoter and cl857ts thermolabile repressor. Plasmid vectors available from the American Type Culture Collection which incorporate derivatives of the λ P_L promoter include plasmid pHUB2, resident in *E. coli* strain JMB9 (ATCC 37092) and pPLc28, resident in *E. coli* RR1 (ATCC 53082).

Recombinant G-CSFR proteins may also be expressed in yeast hosts, preferably from the *Saccharomyces* species, such as *S. cerevisiae*. Yeast of other genera, such as *Pichia* or *Kluyveromyces* may also be employed. Yeast vectors will generally contain an origin of replication from the 2 μ yeast plasmid or an autonomously replicating sequence (ARS), promoter, DNA encoding G-CSFR, sequences for polyadenylation and transcription termination and a selection gene. Preferably, yeast vectors will include an origin of replication and selectable marker permitting transformation of both yeast and *E. coli*, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* trp1 gene, which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, and a promoter derived from a highly expressed yeast gene to induce transcription of a structural sequence downstream. The presence of the trp1 lesion in the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoter sequences in yeast vectors include the promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as

enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman et al., EPA 73,657.

5 Preferred yeast vectors can be assembled using DNA sequences from pBR322 for selection and replication in *E. coli* (Amp^r gene and origin of replication) and yeast DNA sequences including a glucose-repressible ADH2 promoter and α -factor secretion leader. The ADH2 promoter has been described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). The yeast α -factor leader, which directs secretion of heterologous proteins, can be inserted between the promoter and the structural gene to be expressed. See, e.g., Kurjan et al., *Cell* 30:933, 1982; and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. The leader sequence may be modified to contain, near its 3' end, one or more useful restriction sites to facilitate fusion of the leader sequence to foreign genes.

Suitable yeast transformation protocols are known to those of skill in the art; an exemplary technique is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978, selecting for Trp⁺ transformants in a selective medium consisting of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μ g/ml adenine and 20 μ g/ml uracil.

Host strains transformed by vectors comprising the ADH2 promoter may be grown for expression in a rich medium consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 μ g/ml adenine and 80 μ g/ml uracil. Derepression of the ADH2 promoter occurs upon exhaustion of medium glucose. Crude yeast supernatants are harvested by filtration and held at 4°C prior to further purification.

20 Various mammalian or insect cell culture systems can be employed to express recombinant protein. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988). Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, described by Gluzman (*Cell* 23:175, 1981), and other cell lines capable of expressing an appropriate vector including, for example, L cells, C127, 3T3, Chinese hamster ovary (CHO), HeLa and BHK cell lines. Mammalian expression vectors may comprise nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences.

The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells may be provided by viral sources. For example, commonly used promoters and enhancers are derived from Polyoma, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites may be used to provide the other genetic elements required for expression of a heterologous DNA sequence. The early and late promoters are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., *Nature* 273:113, 1978). Smaller or larger SV40 fragments may also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* I site located in the viral origin of replication is included. Further, mammalian genomic G-CSFR promoter, control and/or signal sequences may be utilized, provided such control sequences are compatible with the host cell chosen. Additional details regarding the use of a mammalian high expression vector to produce a recombinant mammalian G-CSF receptor are provided in Example 2 below. Exemplary vectors can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983).

45 A useful system for stable high level expression of mammalian receptor cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986).

A particularly preferred eukaryotic vector for expression of G-CSFR DNA is disclosed below in Example 2. This vector, referred to as pCAV/NOT, was derived from the mammalian high expression vector pDC201 and contains regulatory sequences from SV40, adenovirus-2, and human cytomegalovirus.

50 Purified mammalian G-CSF receptors or analogs are prepared by culturing suitable host/vector systems to express the recombinant translation products of the DNAs of the present invention, which are then purified from culture media or cell extracts.

For example, supernatants from systems which secrete recombinant protein into culture media can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a suitable purification matrix. For example, a suitable affinity matrix can comprise a G-CSF or lectin or antibody molecule bound to a suitable support. Alternatively, an anion exchange resin can be employed, for

example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Sulfopropyl groups are preferred.

Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify a G-CSFR composition. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a homogeneous recombinant protein.

Recombinant protein produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more concentration, salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of recombinant mammalian G-CSFR can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Fermentation of yeast which express mammalian G-CSFR as a secreted protein greatly simplifies purification. Secreted recombinant protein resulting from a large-scale fermentation can be purified by methods analogous to those disclosed by Urdal et al. (*J. Chromatog.* 296:171, 1984). This reference describes two sequential, reversed-phase HPLC steps for purification of recombinant human GM-CSF on a preparative HPLC column.

Human G-CSFR synthesized in recombinant culture is characterized by the presence of non-human cell components, including proteins, in amounts and of a character which depend upon the purification steps taken to recover human G-CSFR from the culture. These components ordinarily will be of yeast, prokaryotic or non-human higher eukaryotic origin and preferably are present in innocuous contaminant quantities, on the order of less than 1 percent by weight. Further, recombinant cell culture enables the production of G-CSFR free of proteins which may be normally associated with G-CSFR as it is found in nature in its species of origin, e.g. in cells, cell exudates or body fluids.

G-CSFR compositions are prepared for administration by mixing G-CSFR having the desired degree of purity with physiologically acceptable carriers. Such carriers will be nontoxic to recipients at the dosages and concentrations employed. Ordinarily, the preparation of such compositions entails combining the G-CSFR with buffers, antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, proteins, amino acids, carbohydrates including glucose, sucrose or dextrans, chelating agents such as EDTA, glutathione and other stabilizers and excipients.

G-CSFR compositions may be used to attenuate G-CSF-mediated immune responses. To achieve this result, a therapeutically effective quantity of a G-CSFR composition is administered to a mammal, preferably a human, in association with a pharmaceutical carrier or diluent.

The following examples are offered by way of illustration, and not by way of limitation.

EXAMPLES

Example 1

Binding Assays

A. Radiolabeling of G-CSF. Recombinant human G-CSF, in the form of a fusion protein containing a hydrophilic octapeptide at the N-terminus, was expressed in yeast as a secreted protein and purified by affinity chromatography as described by Hopp et al., *BioTechnology* 6:1204, 1988. The protein was radiolabeled using the commercially available solid phase agent, IODO-GEN (Pierce). In this procedure, 5 μ g of IODO-GEN were plated at the bottom of a 10 X 75 mm glass tube and incubated for 20 minutes at 4°C with 75 μ l of 0.1 M sodium phosphate, pH 7.4 and 20 μ l (2 mCi) Na ¹²⁵I. This solution was then transferred to a second glass tube containing 5 μ g G-CSF in 45 μ l PBS for 20 minutes at 4°C. The reaction mixture was fractionated by gel filtration on a 2 ml bed volume of Sephadex G-25 (Sigma) equilibrated in Roswell Park Memorial Institute (RPMI) 1640 medium containing 2.5% (w/v) bovine serum albumin (BSA), 0.2% (w/v) sodium azide and 20 mM Hepes pH 7.4 (binding medium). The final pool of ¹²⁵I-G-CSF was diluted to a working stock solution of 1×10^{-7} M in binding medium and stored for up to one month at 4°C without detectable loss of receptor binding activity. The specific activity is routinely 1×10^{16} cpm/mmol G-CSF. Radiolabeled G-CSF is used as described below to assay for G-CSF receptors.

B. Membrane Binding Assays. Human placental membranes were incubated at 4°C for 2 hr with ¹²⁵I-G-CSF in binding medium, 0.1% bacitracin, 0.02% aprotinin, and 0.4% BSA in a total volume of 1.2 ml.

Control tubes containing in addition a 100 x molar excess of unlabeled G-CSF were also included to determine non-specific binding. The reaction mixture was then centrifuged at 15,000x g in a microfuge for 5 minutes. Supernatants were discarded, the surface of the membrane pellets carefully rinsed with ice-cold binding medium, and the radioactivity counted on a gamma counter. Using this assay, it was determined

that the G-CSFR present in the COS cell supernatants of Example 2 had a K_a of about $1 \times 10^9 \text{ M}^{-1}$ and a molecular weight of about 35 kDa.

C. **Solid Phase Binding Assays.** The ability of G-CSFR to be stably adsorbed to nitrocellulose from detergent extracts of human cells yet retain G-CSF-binding activity provided a means of detecting G-CSFR. Cells extracts were prepared by mixing a cell pellet with a 2X volume of PBS containing 1% Triton X-100 and a cocktail of protease inhibitors (2 mM phenylmethyl sulfonyl fluoride, 10 μM pepstatin, 10 μM leupeptin, 2 mM o-phenanthroline and 2 mM EGTA) by vigorous vortexing. The mixture was incubated on ice for 30 minutes after which it was centrifuged at 12,000x g for 15 minutes at 8°C to remove nuclei and other debris. Two microliter aliquots of cell extracts were placed on dry BA85/21 nitrocellulose membranes (Schleicher and Schuell, Keene, NH) and allowed to dry. The membranes were incubated in tissue culture dishes for 30 minutes in Tris (0.05 M) buffered saline (0.15 M) pH 7.5 containing 3% w/v BSA to block nonspecific binding sites. The membrane was then covered with 0.3 nM ^{125}I -G-CSF in PBS + 3% BSA and incubated for 2 hr at 4°C with shaking. At the end of this time, the membranes were washed 3 times in PBS, dried and placed on Kodak X-Omat AR film for 18 hr at -70°C. This assay was performed to detect the presence of G-CSFR in various cells lines and tissue sources.

D. **Binding Assay for Soluble G-CSFR.** Soluble G-CSFR present in COS-7 cell supernatants are measured by inhibition of ^{125}I -CSF binding to a G-CSF-dependent cell line, or any other human cell or cell line expressing G-CSF receptors, such as as human placental cell. Supernatants are harvested from COS-7 cells 3 days after transfection, concentrated 10-fold, and preincubated with ^{125}I -G-CSF for 1 hour at 37°C. Appropriate G-CSF-receptor-bearing cells are added to a final volume of 150 μl , incubated for an additional 30 minutes at 37°C, and assayed and analyzed as described by Park et al., *J. Biol. Chem.* 261:4177 (1986).

Example 2

Isolation of Human G-CSF R cDNAs by Direct Expression of Active Protein in COS-7 Cells

A tissue source for G-CSFR was selected by screening various human cell lines and tissues for expression of G-CSFR based on their ability to bind ^{125}I -labeled G-CSF, prepared as described above in Example 1A. Human placental membranes were found to express a reasonable number of receptors. Equilibrium binding studies were performed according to Example 1B and showed that the membrane exhibited biphasic binding of ^{125}I -G-CSF with high affinity sites ($K_a = 4 \times 10^{19} \text{ M}^{-1}$) of 0.4 pmoles receptor/mg protein.

An unsized cDNA library was constructed by reverse transcription of polyadenylated mRNA isolated from total RNA extracted from the human placental tissue (Ausubel et al., eds., *Current Protocols in Molecular Biology*, Vol. 1, 1987). The cells were harvested by lysing the tissue cells in a guanidinium isothiocyanate solution and total RNA was isolated using standard techniques as described by Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1982.

Polyadenylated RNA was isolated by oligo dT cellulose chromatography and double-stranded cDNA was prepared by a method similar to that of Gubler and Hoffman, *Gene* 25:263, 1983. Briefly, the polyadenylated RNA was converted to an RNA-cDNA hybrid with reverse transcriptase using oligo dT as a primer. The RNA-cDNA hybrid was then converted into double-stranded cDNA using RNAase H in combination with DNA polymerase I. The resulting double stranded cDNA was blunt-ended with T4 DNA polymerase. *Bgl*II adaptors were ligated to the 5' ends of the resulting blunt-ended cDNA as described by Haymerle, et al., *Nuclear Acids Research*, 14: 8615, 1986. The non-ligated adaptors were removed by gel filtration chromatography at 68°C, leaving 24 nucleotide non-self-complementary overhangs on the cDNA. The same procedure was used to convert the 5' *Bgl*II ends of the mammalian expression vector pscCAV to 24 nucleotide overhangs complementary to those added to the cDNA. Optimal proportions of adapted vector and cDNA were ligated in the presence of T4 polynucleotide kinase. Dialyzed ligation mixtures were electroporated into *E. coli* strain DH5 α and transformants selected on ampicillin plates.

The resulting cDNAs were ligated into the eukaryotic expression vector pscCAV, which was designed to express cDNA sequences inserted at its multiple cloning site when transfected into mammalian cells. pscCAV was assembled from pDC201 (a derivative of pMLSV, previously described by Cosman et al., *Nature* 312: 768, 1984), SV40 and cytomegalovirus DNA and comprises, in sequence with the direction of

transcription from the origin of replication: (1) SV40 sequences from coordinates 5171-5270 containing the origin of replication, enhancer sequences and early and late promoters; (2) cytomegalovirus sequences containing the promoter and enhancer regions (nucleotides 671 to +63 from the sequence published by Boechart et al. (*Cell* 41:521, 1985); (3) adenovirus-2 sequences from coordinates 5779-6079 containing sequences for the motor late promoter and the first exon of the tripartite leader (TPL), coordinates 7101-7172 and 9634-9693 containing the second exon and part of the third exon of the TPL and a multiple cloning site (MCS) containing sites for XhoI, KpnI, SmaI and BglI; (4) SV40 sequences from coordinates 4127-4100 and 2770-2533 containing the polyadenylation and termination signals for early transcription; (5) with adenovirus sequences from coordinates 10532-11156 of the virus-associated RNA genes VAI and VAI1 of pDC201; and (6) pBR322 sequences from coordinates 4363-2486 and 1094-375 containing the ampicillin resistance gene and origin of replication.

The resulting human placental cDNA library in sfCAV was used to transform *E. coli* strain DH5 α , and recombinants were plated to provide approximately 500-600 colonies per plate and sufficient plates to provide approximately 30,000 total colonies per screen. Colonies were scraped from each plate, pooled, and plasmid DNA prepared from each pool. The pooled DNA was then used to transfect a sub-confluent layer of monkey COS-7 cells using DEAE-dextran followed by chloroquine treatment, as described by Luthman et al., *Nucl. Acids Res.* 11:1295 (1983) and McCutchan et al., *J. Natl. Cancer Inst.* 41:351 (1986). The cells were then grown in culture for three days to permit transient expression of the inserted sequences. After three days, cell culture supernatants were discarded and the cell monolayers in each plate assayed for G-CSF binding as follows. Three ml of binding medium containing 1.2×10^{-11} M 125 I-labeled flag-G-CSF was added to each plate and the plates incubated at 4°C for 120 minutes. This medium was then discarded, and each plate was washed once with cold binding medium (containing no labeled G-CSF) and twice with cold PBS. The edges of each plate were then broken off, leaving a flat disk which was contacted with X-ray film for 72 hours at -70°C using an intensifying screen. G-CSF binding activity was visualized on the exposed films as a dark spot against a relatively uniform background.

After approximately 30,000 recombinants from the library had been screened in this manner, nine transfectant pools were observed to provide G-CSF binding foci which were clearly apparent against the background exposure.

A frozen stock of bacteria from the positive pool was then used to obtain plates of approximately 60 colonies. Replicas of these plates were made on nitrocellulose filters, and the plates were then scraped and plasmid DNA prepared and transfected as described above to identify a positive plate. Bacteria from individual colonies from the nitrocellulose replica of this plate were grown in 0.2 ml cultures, which were used to obtain plasmid DNA. The plasmid DNA was then transfected into COS-7 cells as described above. In this manner, a single clone, clone D-7, was isolated which was capable of inducing expression of G-CSFR in COS cells. A glycerol stock of bacteria transformed with this G-CSFR cDNA clone in the expression vector pCAV/NOT (or pDC302) has been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852, USA, under accession number 68102.

An additional cDNA clone encoding G-CSFR was isolated from the same placental library. Recombinants from the placental cDNA library were plated on *E. coli* strain DH5 α and transformants selected on ampicillin plates. The transformants were screened by plaque hybridization techniques under conditions of high stringency (63°C, 0.2X SSC) using a 32 P-labeled probe made from the human G-CSFR clone D-7. A hybridizing clone (clone 25-1) was isolated which is identical to clone D-7, except that it contains an intron insertion after nucleotide 2411, adding nucleotides 2412-2832 of Figure 6 and resulting in a change in reading frame and a corresponding change in amino acid sequence. The 3' nucleotide sequence and predicted C-terminal amino acid sequence of clone 25-1 are set forth in Figure 6.

Example 3

Construction of cDNAs Encoding Soluble Human G-CSFR

Soluble human G-CSFR was cloned into the mammalian expression vector pDC302, described above, utilizing the polymerase chain reaction (PCR) technique. The following primers were used:

5' End Primer

5'-GGTACCATGGCAAGGCTGGGAAAC
Asp718 site/Initiation Codon

3' End Primer5'-TCTAGAACTCAGCCTCGATGTG

BglII/Termination Codon

5

The PCT product thus contains Asp718 and BglII restriction sites at the 5' and 3' termini, respectively. These restriction sites are used to clone into pDC302. The 3' sequence is antisense relative to sequence disclosed in Figures 2-5. The template for the PCR reaction is clone 25-1, described above, which contains
 10 the G-CSFR. The DNA sequences encoding the G-CSFR are then amplified by PCR, substantially as described by Innis et al., eds., *PCR Protocols: A Guide to Methods and Applications* (Academic Press, 1990). The resulting amplified clone was then isolated and ligated into pDC302 and expressed in monkey COS-7 cells as described above.

15 **Example 4**Preparation of Monoclonal Antibodies to G-CSFR

Preparations of purified recombinant G-CSFR, for example, human G-CSFR, or transfected COS cells
 20 expressing high levels of G-CSFR are employed to generate monoclonal antibodies against G-CSFR using conventional techniques, for example, those disclosed in U.S. Patent 4,411,993. Such antibodies are likely to be useful in interfering with G-CSF binding to G-CSF receptors, for example, in ameliorating toxic or other undesired effects of G-CSF, or as components of diagnostic or research assays for G-CSF or soluble G-CSF receptor.

25 To immunize mice, G-CSFR immunogen is emulsified in complete Freund's adjuvant and injected in amounts ranging from 10-100 µg subcutaneously into Balb/c mice. Ten to twelve days later, the immunized animals are boosted with additional immunogen emulsified in incomplete Freund's adjuvant and periodically boosted thereafter on a weekly to biweekly immunization schedule. Serum samples are periodically taken by retro-orbital bleeding or tail-tip excision for testing by dot-blot assay (antibody sandwich) or ELISA
 30 (enzyme-linked immunosorbent assay). Other assay procedures are also suitable. Following detection of an appropriate antibody titer, positive animals are given an intravenous injection of antigen in saline. Three to four days later, the animals are sacrificed, splenocytes harvested, and fused to the murine myeloma cell line NS1. Hybridoma cell lines generated by this procedure are plated in multiple microtiter plates in a HAT selective medium (hypoxanthine, aminopterin, and thymidine) to inhibit proliferation of non-fused cells,
 35 myeloma hybrids, and spleen cell hybrids.

Hybridoma clones thus generated can be screened by ELISA for reactivity with G-CSFR, for example, by adaptations of the techniques disclosed by Engvall et al., *Immunochem.* 8:871 (1971) and in U.S. Patent 4,703,004. Positive clones are then injected into the peritoneal cavities of syngeneic Balb/c mice to produce ascites containing high concentrations (>1 mg/ml) of anti-G-CSFR monoclonal antibody. The resulting
 40 monoclonal antibody can be purified by ammonium sulfate precipitation followed by gel exclusion chromatography, and/or affinity chromatography based on binding of antibody to Protein A of *Staphylococcus aureus*.

Claims

45

1. An isolated DNA sequence comprising a DNA sequence encoding a biologically active mammalian G-CSF receptor (G-CSFR) protein comprising the sequence of amino acids 1-603 of Figures 2-5.
2. A DNA sequence selected from the group consisting of:
 - 50 (a) cDNA clones comprising a nucleotide sequence derived from the coding region of a native mammalian G-CSFR gene according to claim 1;
 - (b) DNA sequences capable of hybridization to the clones of (a) under moderately stringent conditions (50 °C, 2 x SSC) and which encode biologically active G-CSFR molecules; and
 - (c) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences
 55 defined in (a) and (b) and which encode biologically active G-CSFR molecules.
3. An isolated DNA sequence according to claim 1, encoding a soluble biologically active mammalian G-CSFR.

4. A recombinant expression vector comprising an DNA sequence according to claim 1.
5. A recombinant expression vector comprising a DNA sequence according to claim 2.
- 5 6. A recombinant expression vector comprising a DNA sequence according to claim 3.
7. A process for preparing a mammalian G-CSF receptor or an analog thereof, comprising culturing a suitable host cell comprising a vector according to claim 4 under conditions promoting expression.
- 10 8. A purified biologically active mammalian G-CSF receptor composition comprising the sequence of amino acids 1-603 of Figures 2-5.
9. A purified biologically active mammalian G-CSF receptor composition according to claim 8, consisting essentially of human G-CSF receptor.
- 15 10. A composition for regulating immune or inflammatory responses in a mammal, comprising an effective amount of a mammalian G-CSF receptor protein composition according to claim 8, and a suitable diluent or carrier.
- 20 11. Use of a composition according to Claim 8 for the manufacture of a medicament for regulating immune responses in a mammal.
12. An assay method for detection of G-CSF or G-CSF receptor molecules or the interaction thereof, comprising use of protein composition according to claim 8.
- 25 13. Antibodies immunoreactive with mammalian G-CSF receptors encoded by a DNA sequence of claim 2.
14. A purified biologically active mammalian G-CSF receptor composition according to claim 9, wherein the G-CSF receptor is a soluble G-CSF receptor.

Patentansprüche

1. Isolierte DNA-Sequenz, umfassend eine DNA-Sequenz, die für ein biologisch aktives Säuger-G-CSF-Rezeptor(G-CSFR)-Protein kodiert, welches die Sequenz der Aminosäuren 1-603 der Figuren 2-5 umfaßt.
2. DNA-Sequenz, ausgewählt aus der Gruppe bestehend aus:
 - (a) cDNA-Klonen, umfassend eine Nukleotidsequenz, die von der kodierenden Region eines nativen Säuger-G-CSFR-Gens nach Anspruch 1 abgeleitet ist;
 - 40 (b) DNA-Sequenzen, die mit den Klonen von (a) unter mäßig stringenter Bedingungen (50 °C, 2 x SSC) hybridisieren können und die für biologisch aktive G-CSFR-Moleküle kodieren; und
 - (c) DNA-Sequenzen, die infolge des genetischen Kodes eine Degenerierung der DNA-Sequenzen, die in (a) und (b) definiert sind, darstellen und die für biologisch aktive G-CSFR-Moleküle kodieren.
- 45 3. Isolierte DNA-Sequenz nach Anspruch 1, welche für einen löslichen biologisch aktiven Säuger-G-CSFR kodiert.
4. Rekombinanter Expressionsvektor, umfassend eine DNA-Sequenz nach Anspruch 1.
- 50 5. Rekombinanter Expressionsvektor, umfassend eine DNA-Sequenz nach Anspruch 2.
6. Rekombinanter Expressionsvektor, umfassend eine DNA-Sequenz nach Anspruch 3.
7. Verfahren zum Herstellen eines Säuger-G-CSF-Rezeptors oder eines Analogons davon, umfassend das Kultivieren einer geeigneten Wirtszelle, die einen Vektor nach Anspruch 4 umfaßt, unter Bedingungen, welche die Expression fördern.

8. Gereinigte biologisch aktive Säuger-G-CSF-Rezeptor-Zusammensetzung, umfassend die Sequenz der Aminosäuren 1-603 der Figuren 2-5.
9. Gereinigte biologisch aktive Säuger-G-CSF-Rezeptor-Zusammensetzung nach Anspruch 8, bestehend
5 im wesentlichen aus humanem G-CSF-Rezeptor.
10. Zusammensetzung zum Regulieren von Immun- oder Entzündungsreaktionen in einem Säuger, umfassend eine wirksame Menge einer Säuger-G-CSF-Rezeptor-Protein-Zusammensetzung nach Anspruch 8, und ein geeignetes Verdünnungsmittel oder einen geeigneten Träger.
11. Verwendung einer Zusammensetzung nach Anspruch 8 bei der Herstellung eines Arzneimittels zum Regulieren von Immunreaktionen in einem Säuger.
12. Testverfahren zum Nachweis von G-CSF oder G-CSF-Rezeptor-Molekülen oder der Wechselwirkung
15 davon, umfassend die Verwendung der Proteinzusammensetzung nach Anspruch 8.
13. Antikörper, die mit Säuger-G-CSF-Rezeptoren, für die eine DNA-Sequenz nach Anspruch 2 kodiert, eine Immunreaktion eingehen können.
14. Gereinigte biologisch aktive Säuger-G-CSF-Rezeptor-Zusammensetzung nach Anspruch 9, worin der G-CSF-Rezeptor ein löslicher G-CSF-Rezeptor ist.

Revendications

1. Séquence d'ADN isolée comprenant une séquence d'ADN codant pour une protéine consistant en un récepteur de G-CSF de mammifère biologiquement actif (G-CSFR) comprenant la séquence des amino-acides 1-603 des figures 2-5.
2. Séquence d'ADN choisie dans le groupe consistant en :
30 (a) des clones d'ADNc comprenant une séquence de nucléotides dérivée de la région codante d'un gène de G-CSFR naturel de mammifère suivant la revendication 1 ;
(b) des séquences d'ADN aptes à l'hybridation avec les clones de (a) dans des conditions modérément drastiques (50 °C, SSC 2 x) et codant pour des molécules de G-CSFR biologiquement actives ; et
35 (c) des séquences d'ADN qui, en résultat du code génétique, sont dégénérées en les séquences d'ADN définies en (a) et (b) et qui codent pour des molécules de G-CSFR biologiquement actives.
3. Séquence d'ADN isolée suivant la revendication 1, codant pour un G-CSFR biologiquement actif soluble de mammifère.
4. Vecteur d'expression recombinant comprenant une séquence d'ADN suivant la revendication 1.
5. Vecteur d'expression recombinant comprenant une séquence d'ADN suivant la revendication 2.
6. Vecteur d'expression recombinant comprenant une séquence d'ADN suivant la revendication 3.
7. Procédé de préparation d'un récepteur de G-CSF de mammifère ou d'un de ses analogues, comprenant la culture d'une cellule-hôte convenable comprenant un vecteur suivant la revendication 4 dans des conditions favorisant l'expression.
8. Composition de récepteur de G-CSF biologiquement actif purifié de mammifère, comprenant la séquence des amino-acides 1-603 des figures 2-5.
9. Composition de récepteur de G-CSF biologiquement actif purifié de mammifère suivant la revendication 8, consistant essentiellement en récepteur de G-CSF humain.
10. Composition pour la régulation de réponses immunitaires ou inflammatoires chez un mammifère, comprenant une quantité efficace d'une composition de protéine consistant en un récepteur de G-CSF

de mammifère suivant la revendication 8, et un diluant ou support convenable.

11. Utilisation d'une composition suivant la revendication 8 pour la production d'un médicament destiné à la régulation de réponses immunitaires chez un mammifère.

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12. Méthode d'analyse pour la détection de molécules de G-CSF ou de molécules de récepteur de G-CSF ou de leur interaction, comprenant l'utilisation de la composition de protéine suivant la revendication 8.

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13. Anticorps immunoréactifs avec des récepteurs de G-CSF de mammifères codés par une séquence d'ADN suivant la revendication 2.

14. Composition de récepteur de G-CSF biologiquement actif purifié de mammifère suivant la revendication 9, dans laquelle le récepteur de G-CSF est un récepteur de G-CSF soluble.

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FIGURE 1

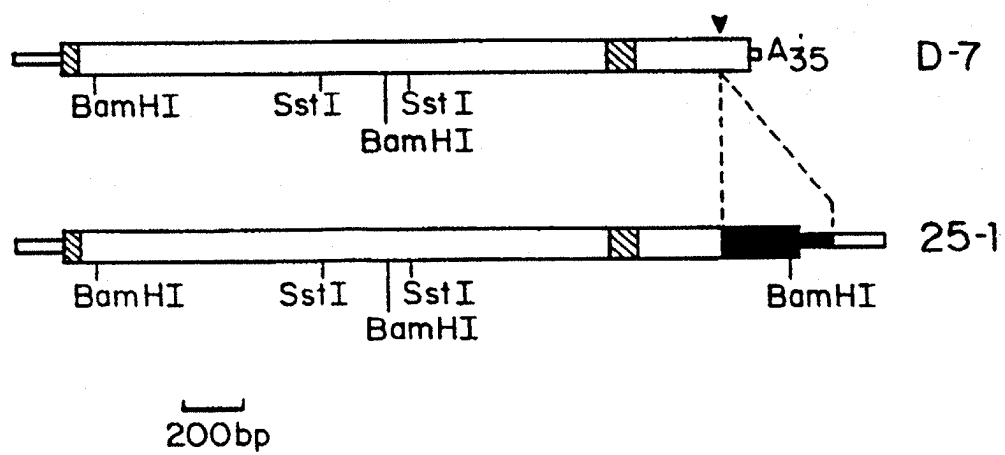


FIG. 2

						TG	GAC	TGC	AGC	TGG	TTT	CAG	GAA	CTT	CTC	TTG	32
ACG	AGA	AGA	GAG	ACC	AAG	GAG	GCC	AAG	CAG	GGG	CTG	GGC	CAG	AGG	TGC		80
CAA	CAT	GGG	GAA	ACT	GAG	GCT	CGG	CTC	GGA	AAG	GTG	AAG	TAA	CTT	GTC		128
CAA	GAT	CAC	AAA	GCT	GGT	GAA	CAT	CAA	GTT	GGT	GCT	ATG	GCA	AGG	CTG		176
												Met	Ala	Arg	Leu		
												-24					
GGA	AAC	TGC	AGC	CTG	ACT	TGG	GCT	GCC	CTG	ATC	ATC	CTG	CTG	CTC	CCC		224
Gly	Asn	Cys	Ser	Leu	Thr	Trp	Ala	Ala	Leu	Ile	Ile	Leu	Leu	Leu	Pro		-20
																	-15
GGA	AGT	CTG	GAG	GAG	TGC	GGG	CAC	ATC	AGT	GTC	TCA	GCC	CCC	ATC	GTC		272
Gly	Ser	Leu	Glu	Glu	Cys	Gly	His	Ile	Ser	Val	Ser	Ala	Pro	Ile	Val		
																	1
CAC	CTG	GGG	GAT	CCC	ATC	ACA	GCC	TCC	TGC	ATC	ATC	AAG	CAG	AAC	TGC		320
His	Leu	Gly	Asp	Pro	Ile	Thr	Ala	Ser	Cys	Ile	Ile	Lys	Gln	Asn	Cys		
																	15
AGC	CAT	CTG	GAC	CCG	GAG	CCA	CAG	ATT	CTG	TGG	AGA	CTG	GGA	GCA	GAG		368
Ser	His	Leu	Asp	Pro	Glu	Pro	Gln	Ile	Leu	Trp	Arg	Leu	Gly	Ala	Glu		
																	30
CTT	CAG	CCC	GGG	GGC	AGG	CAG	CAG	CGT	CTG	TCT	GAT	GGG	ACC	CAG	GAA		416
Leu	Gln	Pro	Gly	Gly	Arg	Gln	Gln	Arg	Leu	Ser	Asp	Gly	Thr	Gln	Glu		45
																	50
TCT	ATC	ATC	ACC	CTG	CCC	CAC	CTC	AAC	CAC	ACT	CAG	GCC	TTT	CTC	TCC		464
Ser	Ile	Ile	Thr	Leu	Pro	His	Leu	Asn	His	Thr	Gln	Ala	Phe	Leu	Ser		
																	65
TGC	TGC	CTG	AAC	TGG	GGC	AAC	AGC	CTG	CAG	ATC	CTG	GAC	CAG	GTT	GAG		512
Cys	Cys	Leu	Asn	Trp	Gly	Asn	Ser	Leu	Gln	Ile	Leu	Asp	Gln	Val	Glu		
																	80
CTG	CGC	GCA	GGC	TAC	CCT	CCA	GCC	ATA	CCC	CAC	AAC	CTC	TCC	TGC	CTC		560
Leu	Arg	Ala	Gly	Tyr	Pro	Pro	Ala	Ile	Pro	His	Asn	Leu	Ser	Cys	Leu		
																	95
ATG	AAC	CTC	ACA	ACC	AGC	AGC	CTC	ATC	TGC	CAG	TGG	GAG	CCA	GGA	CCT		608
Met	Asn	Leu	Thr	Thr	Ser	Ser	Leu	Ile	Cys	Gln	Trp	Glu	Pro	Gly	Pro		
																	110
GAG	ACC	CAC	CTA	CCC	ACC	AGC	TTC	ACT	CTG	AAG	AGT	TTC	AAG	AGC	CGG		656
Glu	Thr	His	Leu	Pro	Thr	Ser	Phe	Thr	Leu	Lys	Ser	Phe	Lys	Ser	Arg		125
																	130
GGC	AAC	TGT	CAG	ACC	CAA	GGG	GAC	TCC	ATC	CTG	GAC	TGC	GTG	CCC	AAG		704
Gly	Asn	Cys	Gln	Thr	Gln	Gly	Asp	Ser	Ile	Leu	Asp	Cys	Val	Pro	Lys		
																	145
GAC	GGG	CAG	AGC	CAC	TGC	TGC	ATC	CCA	CGC	AAA	CAC	CTG	CTG	TTG	TAC		752
Asp	Gly	Gln	Ser	His	Cys	Cys	Ile	Pro	Arg	Lys	His	Leu	Leu	Leu	Tyr		
																	160
																	165
																	170

FIG. 3

CAG	AAT	ATG	GGC	ATC	TGG	GTG	CAG	GCA	GAG	AAT	GCG	CTG	GGG	ACC	AGC	800
Gln	Asn	Met	Gly	Ile	Trp	Val	Gln	Ala	Glu	Asn	Ala	Leu	Gly	Thr	Ser	
	175						180					185				
ATG	TCC	CCA	CAA	CTG	TGT	CTT	GAT	CCC	ATG	GAT	GTT	GTG	AAA	CTG	GAG	848
Met	Ser	Pro	Gln	Leu	Cys	Leu	Asp	Pro	Met	Asp	Val	Val	Lys	Leu	Glu	
	190					195					200					
CCC	CCC	ATG	CTG	CGG	ACC	ATG	GAC	CCC	AGC	CCT	GAA	GCG	GCC	CCT	CCC	896
Pro	Pro	Met	Leu	Arg	Thr	Met	Asp	Pro	Ser	Pro	Glu	Ala	Ala	Pro	Pro	
205					210					215					220	
CAG	GCA	GGC	TGC	CTA	CAG	CTG	TGC	TGG	GAG	CCA	TGG	CAG	CCA	GGC	CTG	944
Gln	Ala	Gly	Cys	Leu	Gln	Leu	Cys	Trp	Glu	Pro	Trp	Gln	Pro	Gly	Leu	
			225						230					235		
CAC	ATA	AAT	CAG	AAG	TGT	GAG	CTG	CGC	CAC	AAG	CCG	CAG	CGT	GGA	GAA	992
His	Ile	Asn	Gln	Lys	Cys	Glu	Leu	Arg	His	Lys	Pro	Gln	Arg	Gly	Glu	
			240					245					250			
GCC	AGC	TGG	GCA	CTG	GTG	GGC	CCC	CTC	CCC	TTG	GAG	GCC	CTT	CAG	TAT	1040
Ala	Ser	Trp	Ala	Leu	Val	Gly	Pro	Leu	Pro	Leu	Glu	Ala	Leu	Gln	Tyr	
	255						260					265				
GAG	CTC	TGC	GGG	CTC	CTC	CCA	GCC	ACG	GCC	TAC	ACC	CTG	CAG	ATA	CGC	1088
Glu	Leu	Cys	Gly	Leu	Leu	Pro	Ala	Thr	Ala	Tyr	Thr	Leu	Gln	Ile	Arg	
	270					275					280					
TGC	ATC	CGC	TGG	CCC	CTG	CCT	GGC	CAC	TGG	AGC	GAC	TGG	AGC	CCC	AGC	1136
Cys	Ile	Arg	Trp	Pro	Leu	Pro	Gly	His	Trp	Ser	Asp	Trp	Ser	Pro	Ser	
285					290				295						300	
CTG	GAG	CTG	AGA	ACT	ACC	GAA	CGG	GCC	CCC	ACT	GTC	AGA	CTG	GAC	ACA	1184
Leu	Glu	Leu	Arg	Thr	Thr	Glu	Arg	Ala	Pro	Thr	Val	Arg	Leu	Asp	Thr	
				305					310					315		
TGG	TGG	CGG	CAG	AGG	CAG	CTG	GAC	CCC	AGG	ACA	GTG	CAG	CTG	TTC	TGG	1232
Trp	Trp	Arg	Gln	Arg	Gln	Leu	Asp	Pro	Arg	Thr	Val	Gln	Leu	Phe	Trp	
			320					325					330			
AAG	CCA	GTG	CCC	CTG	GAG	GAA	GAC	AGC	GGA	CGG	ATC	CAA	GGT	TAT	GTG	1280
Lys	Pro	Val	Pro	Leu	Glu	Glu	Asp	Ser	Gly	Arg	Ile	Gln	Gly	Tyr	Val	
	335						340					345				
GTT	TCT	TGG	AGA	CCC	TCA	GGC	CAG	GCT	GGG	GCC	ATC	CTG	CCC	CTC	TGC	1328
Val	Ser	Trp	Arg	Pro	Ser	Gly	Gln	Ala	Gly	Ala	Ile	Leu	Pro	Leu	Cys	
	350					355					360					
AAC	ACC	ACA	GAG	CTC	AGC	TGC	ACC	TTC	CAC	CTG	CCT	TCA	GAA	GCC	CAG	1376
Asn	Thr	Thr	Glu	Leu	Ser	Cys	Thr	Phe	His	Leu	Pro	Ser	Glu	Ala	Gln	
365					370					375					380	
GAG	GTG	GCC	CTT	GTG	GCC	TAT	AAC	TCA	GCC	GGG	ACC	TCT	CGC	CCC	ACC	1424
Glu	Val	Ala	Leu	Val	Ala	Tyr	Asn	Ser	Ala	Gly	Thr	Ser	Arg	Pro	Thr	
				385					390					395		

FIG. 4

CCG	GTG	GTC	TTC	TCA	GAA	AGC	AGA	GGC	CCA	GCT	CTG	ACC	AGA	CTC	CAT	1472
Pro	Val	Val	Phe	Ser	Glu	Ser	Arg	Gly	Pro	Ala	Leu	Thr	Arg	Leu	His	
			400					405					410			
GCC	ATG	GCC	CGA	GAC	CCT	CAC	AGC	CTC	TGG	GTA	GGC	TGG	GAG	CCC	CCC	1520
Ala	Met	Ala	Arg	Asp	Pro	His	Ser	Leu	Trp	Val	Gly	Trp	Glu	Pro	Pro	
			415				420					425				
AAT	CCA	TGG	CCT	CAG	GGC	TAT	GTG	ATT	GAG	TGG	GGC	CTG	GGC	CCC	CCC	1568
Asn	Pro	Trp	Pro	Gln	Gly	Tyr	Val	Ile	Glu	Trp	Gly	Leu	Gly	Pro	Pro	
			430			435					440					
AGC	GCG	AGC	AAT	AGC	AAC	AAG	ACC	TGG	AGG	ATG	GAA	CAG	AAT	GGG	AGA	1616
Ser	Ala	Ser	Asn	Ser	Asn	Lys	Thr	Trp	Arg	Met	Glu	Gln	Asn	Gly	Arg	
					450				455						460	
GCC	ACG	GGG	TTT	CTG	CTG	AAG	GAG	AAC	ATC	AGG	CCC	TTT	CAG	CTC	TAT	1664
Ala	Thr	Gly	Phe	Leu	Leu	Lys	Glu	Asn	Ile	Arg	Pro	Phe	Gln	Leu	Tyr	
				465				470						475		
GAG	ATC	ATC	GTG	ACT	CCC	TTG	TAC	CAG	GAC	ACC	ATG	GGA	CCC	TCC	CAG	1712
Glu	Ile	Ile	Val	Thr	Pro	Leu	Tyr	Gln	Asp	Thr	Met	Gly	Pro	Ser	Gln	
			480					485					490			
CAT	GTC	TAT	GCC	TAC	TCT	CAA	GAA	ATG	GCT	CCC	TCC	CAT	GCC	CCA	GAG	1760
His	Val	Tyr	Ala	Tyr	Ser	Gln	Glu	Met	Ala	Pro	Ser	His	Ala	Pro	Glu	
			495				500					505				
CTG	CAT	CTA	AAG	CAC	ATT	GGC	AAG	ACC	TGG	GCA	CAG	CTG	GAG	TGG	GTG	1808
Leu	His	Leu	Lys	His	Ile	Gly	Lys	Thr	Trp	Ala	Gln	Leu	Glu	Trp	Val	
			510			515					520					
CCT	GAG	CCC	CCT	GAG	CTG	GGG	AAG	AGC	CCC	CTT	ACC	CAC	TAC	ACC	ATC	1856
Pro	Glu	Pro	Pro	Glu	Leu	Gly	Lys	Ser	Pro	Leu	Thr	His	Tyr	Thr	Ile	
					530				535						540	
TTC	TGG	ACC	AAC	GCT	CAG	AAC	CAG	TCC	TTC	TCC	GCC	ATC	CTG	AAT	GCC	1904
Phe	Trp	Thr	Asn	Ala	Gln	Asn	Gln	Ser	Phe	Ser	Ala	Ile	Leu	Asn	Ala	
				545				550						555		
TCC	TCC	CGT	GGC	TTT	GTC	CTC	CAT	GGC	CTG	GAG	CCC	GCC	AGT	CTG	TAT	1952
Ser	Ser	Arg	Gly	Phe	Val	Leu	His	Gly	Leu	Glu	Pro	Ala	Ser	Leu	Tyr	
			560					565					570			
CAC	ATC	CAC	CTC	ATG	GCT	GCC	AGC	CAG	GCT	GGG	GCC	ACC	AAC	AGT	ACA	2000
His	Ile	His	Leu	Met	Ala	Ala	Ser	Gln	Ala	Gly	Ala	Thr	Asn	Ser	Thr	
			575				580					585				
GTC	CTC	ACC	CTG	ATG	ACC	TTG	ACC	CCA	GAG	GGG	TCG	GAG	CTA	CAC	ATC	2048
Val	Leu	Thr	Leu	Met	Thr	Leu	Thr	Pro	Glu	Gly	Ser	Glu	Leu	His	Ile	
			590			595					600					
ATC	CTG	GGC	CTG	TTC	GGC	CTC	CTG	CTG	TTG	CTC	ACC	TGC	CTC	TGT	GGA	2096
Ile	Leu	Gly	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Leu	Thr	Cys	Leu	Cys	Gly	
					610					615					620	

FIG. 5

ACT	GCC	TGG	CTC	TGT	TGC	AGC	CCC	AAC	AGG	AAG	AAT	CCC	CTC	TGG	CCA	2144
Thr	Ala	Trp	Leu	Cys	Cys	Ser	Pro	Asn	Arg	Lys	Asn	Pro	Leu	Trp	Pro	
				625					630						635	
AGT	GTC	CCA	GAC	CCA	GCT	CAC	AGC	AGC	CTG	GGC	TCC	TGG	GTG	CCC	ACA	2192
Ser	Val	Pro	Asp	Pro	Ala	His	Ser	Ser	Leu	Gly	Ser	Trp	Val	Pro	Thr	
			640					645						650		
ATC	ATG	GAG	GAG	GAT	GCC	TTC	CAG	CTG	CCC	GGC	CTT	GGC	ACG	CCA	CCC	2240
Ile	Met	Glu	Glu	Asp	Ala	Phe	Gln	Leu	Pro	Gly	Leu	Gly	Thr	Pro	Pro	
		655					660					665				
ATC	ACC	AAG	CTC	ACA	GTG	CTG	GAG	GAG	GAT	GAA	AAG	AAG	CCG	GTG	CCC	2288
Ile	Thr	Lys	Leu	Thr	Val	Leu	Glu	Glu	Asp	Glu	Lys	Lys	Pro	Val	Pro	
	670					675					680					
TGG	GAG	TCC	CAT	AAC	AGC	TCA	GAG	ACC	TGT	GGC	CTC	CCC	ACT	CTG	GTC	2336
Trp	Glu	Ser	His	Asn	Ser	Ser	Glu	Thr	Cys	Gly	Leu	Pro	Thr	Leu	Val	
685					690					695					700	
CAG	ACC	TAT	GTG	CTC	CAG	GGG	GAC	CCA	AGA	GCA	GTT	TCC	ACC	CAG	CCC	2384
Gln	Thr	Tyr	Val	Leu	Gln	Gly	Asp	Pro	Arg	Ala	Val	Ser	Thr	Gln	Pro	
			705					710						715		
CAA	TCC	CAG	TCT	GGC	ACC	AGC	GAT	CAG	GCT	GGG	CCT	CCC	AGG	CGA	TCT	2432
Gln	Ser	Gln	Ser	Gly	Thr	Ser	Asp	Gln	Ala	Gly	Pro	Pro	Arg	Arg	Ser	
			720					725					730			
GCA	TAC	TTT	AAG	GAC	CAG	ATC	ATG	CTC	CAT	CCA	GCC	CCA	CCC	AAT	GGC	2480
Ala	Tyr	Phe	Lys	Asp	Gln	Ile	Met	Leu	His	Pro	Ala	Pro	Pro	Asn	Gly	
		735					740					745				
CTT	TTG	TGC	TTG	TTT	CCT	ATA	ACT	TCA	GTA	TTG	TAA	ACTAGTTTTT				2526
Leu	Leu	Cys	Leu	Phe	Pro	Ile	Thr	Ser	Val	Leu						
		750				755										
GGTTTGCAAA	AAAAAAAAAA															2546

FIG. 6

↓

CAG GTC CTT	TAT GGG CAG CTG CTG	2432
Gln Val Leu Tyr Gly Gln Leu Leu		
750	755	
GGC AGC CCC ACA AGC CCA GGG CCA GGG CAC TAT CTC CGT GTG ACT CCA	2480	
Gly Ser Pro Thr Ser Pro Gly Pro Gly His Tyr Leu Arg Val Thr Pro		
760	765	770
CTC AGC CCC TCT TGG CGG GCC TCA CCC CCA GCC CCA AGT CCT ATG AGA	2528	
Leu Ser Pro Ser Trp Arg Ala Ser Pro Pro Ala Pro Ser Pro Met Arg		
775	780	785
ACC TCT GGT TCC AGG CCA GCC CCT TGG GGA CCC TGG TAA CCC CAG CCC	2576	
Thr Ser Gly Ser Arg Pro Ala Pro Trp Gly Pro Trp		
790	795	800
CAA GCC AGG AGG ACG ACT GTG TCT TTG GGC CAC TGC TCA ACT TCC CCC	2624	
TCC TGC AGG GGA TCC GGG TCC ATG GGA TGG AGG CGC TGG GGA GCT TCT	2672	
AGG GCT TCC TGG GGT TCC CTT CTT GGG CCT GCC TTT TAA AGG CCT GAG	2720	
CTA GCT GGA GAA GAG GGG AGG GTC CAT AAG CCC ATG ACT AAA AAC TAC	2768	
CCC AGC CCA GGC TCT CAC CAT CTC CAG TCA CCA GCA TCT CCC TCT CCT	2816	
↓		
CCC AAT CTC CAT AGG CTG GGC CTC CCA GGC GAT CTG CAT ACT TTA AGG	2864	
ACC AGA TCA TGC TCC ATC CAG CCC CAC CCA ATG GCC TTT TGT GCT TGT	2912	
<u>TTC CTA TAA CTT CAG TATT</u>	2931	